

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 22.0138 Seconds

(without alignments)
1349.183 Million cell updates/sec

Title: US-09-939-537-35

Sequence: 1 PRASALPAPPTGSALPDPTQ.....VISFLKGLGVACVLARTR 58

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	98.6	240	1	CD7_HUMAN
2	96	33.3	762	2	09NGM7
3	85	29.5	359	2	082CF6
4	83.5	29.0	145	2	09VYE7
5	83	28.8	630	2	06PCS2
6	82	28.5	553	2	09VYF9
7	82	28.5	625	2	0722C5
8	81.5	28.3	1149	2	013577
9	81	28.1	421	2	07KTK9
10	81	28.1	512	2	09VMI4
11	81	28.1	779	2	06FTP1
12	81	28.1	3326	2	07T591
13	80.5	28.0	763	2	09XDH2
14	80	27.8	169	2	07YXK4
15	80	27.8	421	2	098274
16	79.5	27.6	801	1	PRDA_HUMAN
17	78	27.1	210	2	07W2Q1
18	78	27.1	227	2	07W0K1
19	78	27.1	227	2	07WDP9
20	78	27.1	3288	2	07T5D9
21	77	26.7	375	2	093066
22	76.5	26.6	710	2	09CAL8
23	76	26.4	210	2	061748
24	76	26.4	3084	2	08U211
25	75.5	26.2	329	2	06N737
26	75.5	26.2	798	2	09QZP2
27	75.5	26.2	1282	2	07Z836
28	75	26.0	237	2	06AC08
29	75	26.0	343	2	07PK73
30	75	26.0	378	2	066MNA
31	75	26.0	426	2	0742S1

32	75	26.0	518	2	Q8MQG8
33	75	26.0	524	2	002123
34	75	26.0	539	2	Q8MCG9
35	75	26.0	878	2	Q8L7M3
36	75	26.0	891	2	Q9ZM08
37	75	26.0	894	2	Q9FYB2
38	74.5	25.9	309	2	Q9P6R1
39	74.5	25.9	554	2	Q8PUH9
40	74.5	25.9	759	2	Q6DW61
41	74.5	25.9	760	2	Q6DW64
42	74.5	25.9	762	1	P15_CHICK
43	74.5	25.9	763	2	Q6DW62
44	74.5	25.9	764	2	Q6DW63
45	74.5	25.9	772	1	Z469_HUMAN

ALIGNMENTS

RESULT 1
CD7_HUMAN STANDARD; PRT; 240 AA.
AC P05564;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE T-cell antigen CD7 precursor (GP40) (T-cell leukemia antigen) (TP41) (leu-9).
GN Name=CD7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8811517; PubMed=3501369;
RA Aruffo A., Seed B.;
RT "Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS RT cell expression system";
RL EMO J. 6:3313-3316(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9110576; PubMed=1703303;
RA Schaubert L.E., Fleener D.B., Kurtzberg J., Haynes B.F., Kaufman R.E.;
RT "Isolation and characterization of the genomic human CD7 gene: structural similarity with the murine Thy-1 gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:603-607(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abriemson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 205-240 FROM N.A.

RA	MEDLINE=91267564; PubMed=1711009;
RX	Yoshikawa K., Seto M., Ueda R., Obara Y., Notake K., Yokochi T.,
RA	Takahashi T.;
RT	"Molecular cloning of the gene coding for the human T cell
RT	differentiation antigen CD7.";
RL	Immunogenetics 33:352-360(1991).
RL	[5]
RP	TOPOLOGY.
RX	MEDLINE=90063052; PubMed=2479685;
RA	Ware R.E., Searce R.M., Dietz M.A., Starmer C.F., Palker T.J.,
RA	Haynes B.F.;
RT	"Characterization of the surface topography and putative tertiary
RT	structure of the human CD7 molecule.";
RL	J. Immunol. 143:3632-3640(1989).
RL	[6]
RP	INTERACTION WITH SCTM1.
RX	MEDLINE=20119303; PubMed=10652336; DOI=10.1074/jbc.275.5.3431;
RY	Llyan S.D., Escobar S., Rousseau A.-M., Armstrong A., Fanslow W.C.;
RT	"Identification of CD7 as a cognate of the human Kl2 (SCTM1)
RT	protein.";
RL	J. Biol. Chem. 275:3431-3437(2000).
CC	-1- FUNCTION: Not yet known.
CC	-1- SUBUNIT: Interacts with SCTM1.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC	-1- DATABASE: NAME=PROW; NOTE=CD guide CD7 entry;
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd7.htm".
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch). -----
DR	EMBL; X06180; CAA29546.1; -.
DR	EMBL; M37271; AAA51953.1; -.
DR	EMBL; BC009283; AAH09283.1; -.
DR	EMBL; BC013297; AAH13297.1; -.
DR	EMBL; D00749; BAA00646.1; -.
DR	EMBL; D00747; BAA00646.1; JOINED.
DR	EMBL; D00748; BAA00646.1; JOINED.
DR	PIR; A39016; A39016.
DR	HSPD; P01607; IEHW.
DR	Genew; HGNC:1695; CD7.
DR	H-invDB; HIX0014252; -.
DR	MIM; 186820; -.
DR	GO; GO:0016021; C:integral to membrane; TAS.
DR	GO; GO:0005624; C:membrane fraction; TAS.
DR	GO; GO:0005886; C:plasma membrane; TAS.
DR	GO; GO:0004872; F:receptor activity; TAS.
DR	GO; GO:0006955; P:immune response; TAS.
DR	GO; GO:0042110; P:T-cell activation; TAS.
DR	GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. ; NMS.
DR	InterPro; IPR007110; Ig-like.
DR	Pfam; PF00047; Ig_1.
DR	SMART; SM00409; IG_1.
DR	PROSITE; PS50835; IG_LIKE; 1.
KW	Antigen; Glycoprotein; Immune response; Immunoglobulin domain;
KW	Lipoprotein; Palmitate; Receptor; Repeat; Signal; T-cell;
KM	Transmembrane.
FT	SIGNAL 1 25
FT	CHAIN 26 240
FT	DOMAIN 26 180 Extracellular (Probable).
FT	TRANSMEM 181 201 Probable.
FT	DOMAIN 202 240 Cytoplasmic (Probable).
FT	DOMAIN 26 130 Ig-like.
FT	DOMAIN 145 180 4 x 9 AA tandem repeats, potential spacer function.
FT	DISULFID 35 142 Potential.
FT	DISULFID 48 114 Potential.

FT	LIPID	198	198	S-palmitoyl cysteine.
FT	CARBOHYD	45	45	N-linked (GLCNAC. . .).
FT	CARBOHYD	96	96	N-linked (GLCNAC. . .).
FT	REPEAT	145	153	1.
FT	REPEAT	154	162	2.
FT	REPEAT	163	171	3.
FT	REPEAT	172	180	4.
SO	SEQUENCE	240 AA;	25409 MM;	EBBCE08279552108 CRC64;

Qy	Query Match	98.6%;	Score 284;	DB 1;	Length 240;
	Best Local Similarity	98.3%;	Pred. No. 6.8e-17;		
	Matches	57;	Conservative 1;	Mismatches 0;	Indels 0;
Db	147	PRASALPAPPTGSALPDPOQTASALPDPPASALPALAVALISFLLGLGIVACVLTART	204		

Q9N9M7	PRELIMINARY;	PRT;	762 AA.
AC	Q9N9M7;		
DT	01-OCT-2000 (Tremblrel. 15. Created)		
DT	01-OCT-2000 (Tremblrel. 15. Last sequence update)		
DT	01-OCT-2003 (Tremblrel. 25. Last annotation update)		
DE	Hypothetical protein IJ302.06.		
GN	Name=IJ302.06;		
OS	Leishmania major.		
OC	Eukaryota; Eukaryozoa; Kinetoplastida; Trypanosomatidae; Leishmania.		
CC	NCBI_TaxID=5664;		
CC	NCBI_TaxID=5664;		
CC	SEQUENCE FROM N.A.		
CC	STRAIN=Friedlin;		
CC	MEDLINE=98146435; PubMed=9477341;		
CC	Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,		
CC	Smith D.F.;		
CC	"A physical map of the leishmania major Friedlin genome.";		
CC	Genome Res. 8:135-145(1998).		
CC	[2]		
CC	SEQUENCE FROM N.A.		
CC	STRAIN=Friedlin;		
CC	Hilbert H., Wedler H., Wedler E., Nuesterhoeft A., Ivens A.C.,		
CC	Quail M., Rajandream M.A., Barrell B.G.;		
CC	Submitted (UTN-2000) to the EMBL/GenBank/DBJ databases.		
CC	EMBL; AL359781; CAB95309.1; -		
CC	Hypothetical protein.		
CC	SEQUENCE 762 AA; 79650 MM; CBA1573FFD0F89 CRC64;		

Qy	Query Match	33.3%;	Score 96;	DB 2;	Length 762;
	Best Local Similarity	39.0%;	Pred. No. 2.5;		
	Matches	16;	Conservative 11;	Mismatches 14;	Indels 0;
Db	378	PRASALPAPPTGSALPDPOQTASALPDPPASALPALAVALIS 41			
		PRASALPAPPTGSALPDPOQTASALPDPPASALPALAVALISFLLGLGIVACVLTARTQ	418		

Q82CF6	PRELIMINARY;	PRT;	369 AA.
AC	Q82CF6;		
DT	01-JUN-2003 (Tremblrel. 24. Created)		
DT	01-JUN-2003 (Tremblrel. 24. Last sequence update)		
DT	01-OCT-2003 (Tremblrel. 25. Last annotation update)		
DE	Hypothetical protein.		
GN	OrderedLocustNames=SAVS394;		
OS	Streptomyces avermitilis.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
CC	Streptomycinae; Streptomycetaceae; Streptomycetes.		
CC	NCBI_TaxID=33903;		
CC	[1]		
CC	SEQUENCE FROM N.A.		
CC	STRAIN=MA-4680;		

RA MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto O., Takahashi C.,
 RA Shinoe M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducting the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto O., Shinoe M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.,
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL: AP005042; BAC73106.1;
 DR GO: GO:0016020; C:membrane; IEA.
 DR InterPro: IPR000620; DUF6.
 DR Pfam: PF00892; DUF6; 2.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 369 AA; 36920 MW; 945D9B79E75A5E2 CRC64;
 Query Match 29.5%; Score 85; DB 2; Length 369;
 Best Local Similarity 47.2%; Pred. No. 12;
 Matches 17; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
 QY 1 PRASALPAPPTGSALEPDPOTASALPDPASALPAA 36
 DB 316 PGAAVPGATATAPASVPTATAPVPGATAPSA 351
 RESULT 4
 QYVE7 PRELIMINARY; PRT; 145 AA.
 AC QYVE7;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
 DE CG12724-PA.
 GN ORFNames=CG12724;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyroidea; Drosophilidae; Drosophila.
 NC NCBI_TaxID=7227;
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer V.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fouts L.C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howard T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalish P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Koditz C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon A., Nuskern D.R., Paclet J.M.,
 RA Palazolo M., Pitsman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri U.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers R.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.B.,
 RA Smith C.D., Tupy J.L., Whitfield B.D., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN RN
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RP [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB003492; AAF48251.1; -.
 DR Intact; QYVE7; -.
 DR FlyBase; FBgn0030470; CG12724.
 SQ SEQUENCE 145 AA; 14524 MW; 12E97DA73AF8319 CRC64;
 Query Match 29.0%; Score 83.5; DB 2; Length 145;
 Best Local Similarity 44.1%; Pred. No. 6.8;
 Matches 26; Conservative 5; Mismatches 21; Indels 7; Gaps 4;
 QY 4 SALPAPT--GSALEPDPOTASALPDPAS--ALPALAV--ISFLGLGAGVCVART 57
 DB 33 SAATATPTASGATPTPSPRS--PAPVAGGMLPPTLGLGLGAGKGVSRRLRT 89
 RESULT 5
 Q6PCS2

```

ID 06PCS2 PRELIMINARY; PRT; 690 AA.
AC 06PCS2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Hypothetical protein zgc:64189.
GN ORFNames=zgc:64189;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toobyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Abbey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schmechel A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059189; AAH59189.1; -
DR ZFIN; ZDB-GENE-040426-1397; zgc:64189.
KW Hypothetical protein.
SQ SEQUENCE 690 AA; 72313 MW; 72E3F6955AFB95B2 CRC64;

Query Match 28.8%; Score 83; DB 2; Length 690;
Best Local Similarity 61.3%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 5 ALPAPPTGSALPDPTASALPDPPAASALPPA 35
Db 358 ALPAPPKLIALPAPRLALPAPRLALPPA 388

RESULT 6
Q9VVF9 PRELIMINARY; PRT; 553 AA.
AC Q9VVF9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RE38286D.
GN ORFNames=CG12723;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

```

```

RA Champe M., Chaver C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.O., Munro J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY119125; AAM50985.1; -
DR FlyBase; FBgn0030459; CG12723.
SQ SEQUENCE 553 AA; 58356 MW; 0FF2A5A1C6512B88 CRC64;

Query Match 28.5%; Score 82; DB 2; Length 553;
Best Local Similarity 41.7%; Pred. No. 30;
Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

Qy 1 PRASALPAPPTGSALPDPTASALPDPPAASALPPA 36
Db 348 PQAPAIPTSPSVGVAVPTVPAPSPPTSGFFPPA 383

RESULT 7
Q722C5 PRELIMINARY; PRT; 625 AA.
AC Q722C5;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG12723-PA.
GN ORFNames=CG12723;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Blazek R.G., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostalin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jaitani M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Furl V., Reese M.G.,
RA Rine B.C., Siden-Klamro I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodagel, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers R.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";

```

```

RL Science 287:2185-2195 (2000).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richard S., Sodergren E.J.,
RA Svitskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Fishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svitskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Ceiniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective."
RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettecourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RN SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE004491; AAF48238.3; -
DR Inctact: Q722C5; -
DR FlyBase: FBgn0030459; CG12723.
SQ SEQUENCE 625 AA; 65250 MW; B82192973CB50E9D CRC64;

Query Match 28.5%; Score 82; DB 2; Length 625;
Best Local Similarity 41.7%; Pred. No. 33;
Matches 15; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

```

```

RA Whitney M.A., Grompe M., Friedberg A.S., Moses R.E.;
RT "Cloning and characterization of a human CDNA (INP1L1) sharing
RT homology with inositol polyphosphate phosphatases."
RL Genomics 29:285-287(1995).
DR EMBL: U36818; AAA96558.1; -
DR HSSP: Q43001; 1192.
DR GO: GO:0004437; F1:inositol or phosphatidylinositol phosphatase. .; NAS.
DR InterPro: IPR005135; Exo_endo_phos.
DR InterPro: IPR000300; IPPC.
DR Pfam: PF03372; Exo_endo_phos; 1.
DR SMART: SM00128; IPFC; 1.
SQ SEQUENCE 1149 AA; 126808 MW; DD3B54397362AA2F CRC64;

Query Match 28.3%; Score 81.5; DB 2; Length 1149;
Best Local Similarity 45.0%; Pred. No. 62;
Matches 27; Conservative 6; Mismatches 16; Indels 11; Gaps 5;

```

1 PRASALPA--PRTG--SALPDQTASALPDPPASALPALAVIS--FLG--LGAGVACV 53

Db 78 PRALAPPALPPTGPSSPLPAPT-----FTAAASAPMGLSTVSHDYKGSYGIDLEAV 133

```

RESULT 9
ID Q7KTK9 PRELIMINARY; PRT; 421 AA.
AC Q7KTK9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE CG5261-PA.
GN ORFNames=CG5261;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitely A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter C., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

```


RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Fried E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celisner S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective."
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RL [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Beutenourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter U., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stepleton W., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review."
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RG Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the 2-oxoacid dehydrogenase family.
 DR EMBL; AB003617; AAF52514.1; -.
 DR HSBP; P10515; IFYC.
 DR InAct; Q9VM14; -.
 DR FlyBase; Fggn0031912; CGS261.
 DR GO; GO:0045254; C:pyruvate dehydrogenase complex; IEA.
 DR GO; GO:0008415; P:acyltansferase activity; IEA.
 DR GO; GO:0004742; F:dihydrodipicolylsine-residue acetyltransferase. . .; IEA.
 DR GO; GO:0005515; P:protein binding; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006096; P:glycolysis; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR001078; 2-oxoacid dh.
 DR InterPro; IPR006257; Acetyltransferase.
 DR InterPro; IPR000089; Biotin lipoyl.
 DR InterPro; IPR004157; E3 binding.
 DR InterPro; IPR011053; Hybrid motif.
 DR InterPro; IPR003016; Hybrid motif.
 DR Pfam; PF00198; 2-oxoacid dh; 1.
 DR Pfam; PF00364; Biotin lipoyl; 1.
 DR Pfam; PF02817; E3 binding; 1.
 DR ProDom; PD001115; 2-oxoacid dh; 1.
 DR TIGRFAMs; TIGR01349; PDHac_cif_mito; 1.
 DR PROSITE; PS00189; LIPOYL; 1.
 KW Acyltransferase; Lipoyl; Transferase.
 SQ SEQUENCE 512 AA; 54251 MW; AFA24470E56102FF CRC64;

Query Match 28.1%; Score 81; DB 2; Length 512;
 Best Local Similarity 47.2%; Pred. No. 34;
 Matches 17; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Db 3 ASALPAPPTGSALPDPTASALPDPPAASALPALA 38
 173 AAAAPPAAPAAAPPAAPAAAPPPPPPAAPAA 208

RESULT 11
 AC 06FTPI PRELIMINARY; PRT; 779 AA.
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Similar to sp|P37370 Saccharomyces cerevisiae YLR337c VRP1.
 GN ORFNames=CAGL0C09689;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=284593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boistrasse A., Boyer J., Cattolico L., Confantieri F., de Daruvar A.,
 RA Despons L., Fadre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Kozul R., Lemaire M., Leduc I., Ma L., Muller H.,
 RA Nicoud J.M., Nikolski M., Oztas S., Ozier-Kalogiropoulos O.,
 RA Pellenz S., Pottier S., Richard G.F., Strub M.L., Suleau A.,
 RA Sweeney D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Weyer M., Zivanovic I., Biotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in Yeasts."
 RL Nature 430:35-44(2004)
 DR EMBL; CR380953; CAG59330.1; -.
 DR InterPro; IPR003124; WH2.
 DR Pfam; PF02205; WH2; 2.
 DR SMART; SM00246; WH2; 2.
 SQ SEQUENCE 779 AA; 75743 MW; C850564FBFA3156B CRC64;

Query Match 28.1%; Score 81; DB 2; Length 779;
 Best Local Similarity 51.2%; Pred. No. 49;
 Matches 22; Conservative 2; Mismatches 17; Indels 2; Gaps 1;

Db 1 PRASALPAPPTGSALPDPTASALPDPPA--ASALPALAVIS 41
 406 PWASAPPAAPPAAPPAAPASMTASAPPAAPPAALAAASMS 448

RESULT 12
 AC 07T591 PRELIMINARY; PRT; 3326 AA.
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Large tegument protein.
 GN Name=UL36;
 OS Cercopithecine herpesvirus 1 (CeHV-1) (Simian herpes B virus).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22607624; PubMed=12721804;
 RA Ohsawa K., Black D.H., Sato H., Rogers K., Eberle R.;
 RT "Sequence and genetic arrangement of the UL region of the monkey B
 RT virus (Cercopithecine herpesvirus 1) genome and comparison with the UL
 RT region of other primate herpesviruses."
 RL Arch. Virol. 148:989-997(2003).
 DR EMBL; AB096160; BAC58076.2; -.
 DR InterPro; IPR006928; Herpes_teg_N.
 DR InterPro; IPR005210; Herpes_teg_N.
 DR Pfam; PF04843; Herpes teg N; 1.
 DR Pfam; PF03586; Herpes UL36; 1.
 SQ SEQUENCE 3326 AA; 34556 MW; 6B53B3860F43CDP0 CRC64;

Query Match 28.1%; Score 81; DB 2; Length 3326;
 Best Local Similarity 50.0%; Pred. No. 1,8e+02;
 Matches 19; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

